SEQUENCE LISTING

<110> Immusol Incorporated
Welch, Peter J.
Barber, Jack R.

<120> Tumor Suppressor Molecules and Methods of Use

<130> 039316-0301

<140> US 09/438,917
<141> 1999-11-12

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 16
<212> RNA
<213> Artificial Sequence

<220>
<223> hairpin ribozyme

<400> 1
accucccccag aacccu 16

<210> 2
<211> 16
<212> RNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (1)...(16)
<223> n = A,U,C or G

<400> 2
agggngucgg ggaggu 16

<210> 3
<211> 16
<212> RNA
<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<400> 3
agaguguaag aaacua 16

<210> 4
<211> 16
<212> RNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (1)...(16)
<223> n = A,U,C or G

<400> 4
uagungucua cacucu 16

<210> 5
<211> 1664
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (103)...(1525)

<400> 5
gcctgatgtc gtcccacgcc gtgccggctc tcaggcgccg gaagtgagct gcgcacggcc 60
ggaagcggcg gacgcaggag gcctcgtgga ggacacagca gc atg gga cag tca 114
Met Gly Gln Ser
1

ggg agg tcc cgg cac cag aag cgc gcc ccg ccc cag gcg cag ctc cgc 162
Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln Ala Gln Leu Arg
5 10 15 20

aac ctc gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga 210
Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg
25 30 35

```
ggc tgc acg ggt cgc aac atc cgg cag ctc agc ctg gac gtg cgg cgg     258

Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg
                    40                  45                  50
gtc atg gag ccc gtc act gcc agc cgt ctg cag gtt cgt aag aag aac     306
Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn
            55                  60                  65
tcg ctg aag gac tgc gtg gca gtg gct ggg ccc ctc ggg gtc aca cac     354
Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His
        70                  75                  80
ttt ctg atc cta gca aaa caa gag acc aat gtc tac ttt aag ctg atg     402
Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr Phe Lys Leu Met
    85                  90                  95                  100
cgc ctc cca gga ggc ccc acc ttg acc ttc cag gtc aag aag tac tcg     450
Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser
                105                 110                 115
ctg gtg cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag     498
Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu
            120                 125                 130
cag cag ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc     546
Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro
        135                 140                 145
cat ggt atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc     594
His Gly Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe
    150                 155                 160
ccc tcc atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc     642
Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys
165                 170                 175                 180
ctc ctc atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac     690
Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His
                185                 190                 195
tat agc atc aaa gtt gtt cct gtg ggc gcg agt cgc ggg atg aag aag     738
Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys
            200                 205                 210
ctg ctc cag gag aag ttc ccc aac atg agc cgc ctg cag gac atc agc     786
Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser
        215                 220                 225
gag ctg ctg gcc acg ggc gcg ggg ctg tcg gag agc gag gca gag cct     834
Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser Glu Ala Glu Pro
    230                 235                 240
```

```
gac ggc gac cac aac atc aca gag ctg cct cag gct gtc gct ggc cgt    882
Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala Val Ala Gly Arg
245                 250                 255                 260

ggc aac atg cgg gcc cag cag agt gca gtg cgg ctc acc gag atc ggc    930
Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly
                265                 270                 275

ccg cgg atg aca ctg cag ctc atc aag gtc cag gag ggc gtc ggg gag    978
Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu Gly Val Gly Glu
            280                 285                 290

ggc aaa gtg atg ttc cac agt ttt gtg agc aag acg gag gag gag ctg   1026
Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr Glu Glu Glu Leu
        295                 300                 305

cag gcc atc ctg gaa gcc aag gag aag aag ctg cgg ctg aag gct cag   1074
Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg Leu Lys Ala Gln
    310                 315                 320

agg cag gcc cag cag gcc cag aat gtg cag cgc aag cag gag cag cgg   1122
Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys Gln Glu Gln Arg
325                 330                 335                 340

gag gcc cac aga aag aag agc ctg gag ggc atg aag aag gca cgg gtc   1170
Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys Lys Ala Arg Val
                345                 350                 355

ggg ggt agt gat gaa gag gcc tct ggg atc cct tca agg acg gcg agc   1218
Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser Arg Thr Ala Ser
            360                 365                 370

ctg gag ttg ggt gag gac gat gat gaa cag gaa gat gat gac atc gag   1266
Leu Glu Leu Gly Glu Asp Asp His Glu Gln Glu Asp Asp Asp Ile Glu
        375                 380                 385

tat ttc tgc cag gcg gtg ggc gag gcg ccc agt gag gac ctg ttc ccc   1314
Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu Asp Leu Phe Pro
    390                 395                 400

gag gcc aag cag aaa cgg ctt gcc aag tct cca ggg cgg aag cgg aag   1362
Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly Arg Lys Arg Lys
405                 410                 415                 420

cgg tgg gaa atg gat cga ggc agg ggt cgc ctt tgt gac cag aag ttt   1410
Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys Asp Gln Lys Phe
                425                 430                 435

ccc aag acc aag gac aag tcc cag gga gcc cag gcc agg cgg ggg ccc   1458
Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala Arg Arg Gly Pro
            440                 445                 450
```

```
aga ggg gct tcc cgg gat ggt ggg cga ggc cgg ggc cga ggc cgc cca   1506
Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly Arg Gly Arg Pro
        455                 460                 465

ggg aag aga gtg gcc tga g cccaagccgc accggagcag cggctggatt       1555
Gly Lys Arg Val Ala  *
    470

gaacgcccca gattggggcc cgagatgtgg ccctcggttt cctttcataa aggagttgtg 1615
tccccagccc ttccactcca gtaaagaact gaattggcaa aaaaaaaaa             1664


<210> 6
<211> 473
<212> PRT
<213> homo sapiens

<400> 6
Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln
 1               5                  10                  15
Ala Gln Leu Arg Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe
            20                  25                  30
Val Phe Thr Arg Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu
        35                  40                  45
Asp Val Arg Arg Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val
    50                  55                  60
Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu
65                  70                  75                  80
Gly Val Thr His Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr
                85                  90                  95
Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val
            100                 105                 110
Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His
        115                 120                 125
Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn
    130                 135                 140
Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala Thr Met Phe
145                 150                 155                 160
Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr
                165                 170                 175
Ile Lys Arg Cys Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu
            180                 185                 190
Asp Phe Arg His Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg
        195                 200                 205
Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu
    210                 215                 220
Gln Asp Ile Ser Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser
225                 230                 235                 240
Glu Ala Glu Pro Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala
                245                 250                 255
```

```
Val Ala Gly Arg Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu
            260                 265                 270
Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu
        275                 280                 285
Gly Val Gly Glu Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr
    290                 295                 300
Glu Glu Glu Leu Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg
305                 310                 315                 320
Leu Lys Ala Gln Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys
                325                 330                 335
Gln Glu Gln Arg Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys
            340                 345                 350
Lys Ala Arg Val Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser
        355                 360                 365
Arg Thr Ala Ser Leu Glu Leu Gly Glu Asp Asp Asp Glu Gln Glu Asp
    370                 375                 380
Asp Asp Ile Glu Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu
385                 390                 395                 400
Asp Leu Phe Pro Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly
                405                 410                 415
Arg Lys Arg Lys Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys
            420                 425                 430
Asp Gln Lys Phe Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala
        435                 440                 445
Arg Arg Gly Pro Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly
    450                 455                 460
Arg Gly Arg Pro Gly Lys Arg Val Ala
465                 470
```

<210> 7
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotides

<221> misc_feature
<222> (1)...(87)
<223> n = A,T,C or G

<400> 7
cgcgtaccag gtaatatacc acggaccgaa gtccgtgtgt ttctctggtn nnnttctnnn 60
nnnnnggatc ctgtttccgc ccggttt 87

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 8
gtccgtggta tattacctgg ta 22

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 9
cgaaaccggg cggaaacagg 20

A1 Cnt

<210> 10
<211> 52
<212> RNA
<213> Artificial Sequence

<220>
<223> hairpin ribozyme

<221> misc_feature
<222> (1)...(52)
<223> n = A,U,C or G

<400> 10
nnnnnnnnag aannnnacca gagaaacaca cguuguggua uauuaccugg ua 52

<210> 11
<211> 27
<212> DNA
<213> homo sapiens

<400> 11
ccatcctaat acgactcact atagggc 27

<210> 12
<211> 43
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (1)...(42)
<223> n = A,T,C or G

<400> 12
cgatgctcct ctagactcga gggtaccacc tccccgacnc cct 43

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
ggccacgcgt cgactagtac ttttttttt ttttttv 38

<210> 14
<211> 20
<212> DNA
<213> homo sapiens

<400> 14
cggctcaccg agatcggccc 20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
ggccacgcgt cgactagtac t 21

<210> 16
<211> 429
<212> PRT
<213> mus musculus

<400> 16

```
Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Asn Arg Ala Gln
 1               5                  10                  15
Ala Gln Leu Arg Asn Leu Glu Ser Tyr Ala Ala Gln Pro His Ser Phe
            20                  25                  30
Val Phe Thr Arg Gly Arg Ala Gly Arg Asn Val Arg Gln Leu Ser Leu
        35                  40                  45
Asp Val Arg Arg Val Met Glu Pro Leu Thr Ala Thr Arg Leu Gln Val
    50                  55                  60
Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu
65                  70                  75                  80
Gly Val Thr His Phe Leu Ile Leu Thr Lys Thr Cys Asn Ser Val Tyr
                85                  90                  95
Leu Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Ile
            100                 105                 110
Ser Lys Tyr Thr Leu Ile Arg Asp Val Val Ser Ser Leu Arg Arg His
        115                 120                 125
Arg Met His Glu Gln Gln Phe Asn His Pro Pro Leu Leu Val Leu Asn
    130                 135                 140
Ser Phe Gly Pro Gln Ala Met His Ile Lys Leu Met Ala Thr Met Phe
145                 150                 155                 160
Gln Asn Leu Phe Pro Ser Ile Asn Val His Thr Val Asn Leu Asn Thr
                165                 170                 175
Ile Lys Arg Cys Leu Leu Ile Asn Tyr Asn Pro Asp Ser Gln Glu Leu
            180                 185                 190
Asp Phe Arg His Tyr Ser Val Lys Val Val Pro Val Gly Ala Ser Arg
        195                 200                 205
Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu
    210                 215                 220
Gln Asp Ile Ser Glu Leu Leu Ala Thr Gly Val Gly Leu Ser Asp Ser
225                 230                 235                 240
Glu Val Glu Pro Asp Gly Glu His Asn Thr Thr Glu Leu Pro Gln Ala
                245                 250                 255
Val Ala Gly Arg Gly Asn Met Gln Ala Gln Gln Ser Ala Val Arg Leu
            260                 265                 270
Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Ile Gln Glu
        275                 280                 285
Gly Val Gly Asn Gly Asn Val Leu Phe His Ser Phe Val His Lys Thr
    290                 295                 300
Glu Glu Glu Leu Gln Ala Ile Leu Ala Ala Lys Glu Glu Lys Leu Arg
305                 310                 315                 320
Leu Lys Ala Gln Arg Gln Asn Gln Gln Ala Glu Asn Leu Gln Phe Ser
                325                 330                 335
Arg Ser Cys Arg Gly Pro Gln Glu Glu Glu Pro Gly Arg His Lys Ala
            340                 345                 350
```

```
Ser Pro Cys Lys Gly Arg Arg Glx Gln Glx Cys Glx Gly Pro Arg Gly
        355                 360                 365
Thr Ala Arg Gly Gln Trp Gly Ala Gly Gln Pro Glu Asp Glu Glu Asp
    370                 375                 380
Asp Ala Glu Tyr Phe Arg Gln Ala Val Gly Glu Glu Pro Asp Glu Asp
385                 390                 395                 400
Leu Phe Pro Thr Ala Ala Lys Arg Arg Arg Gln Gly Gly Leu Leu Ala
                405                 410                 415
Lys Lys Gln Arg Gly Phe Glu Gln Arg Pro Gly Asn Lys
            420                 425
```

<210> 17
<211> 460
<212> PRT
<213> Drosophila

<400> 17

```
Met Gly Gly Lys Lys Lys Val His Pro Lys Thr Arg Thr Ala Ala Phe
 1               5                  10                  15
Lys Ala Ser Glu Pro Ser Glu Ile Val Glu Ala Pro His Ser Phe Val
            20                  25                  30
Ile His Arg Gly Leu Ala Cys Pro Tyr Ile Thr Asp Leu Thr Leu Asp
        35                  40                  45
Phe Arg Arg Ile Met Glu Pro Phe Thr Ala Ser Asn Leu Arg Glu Lys
    50                  55                  60
Arg Met Asn Arg Ile Gln Asp Phe Val Cys Leu Ser Ser Phe Phe His
65                  70                  75                  80
Val Ser His Met Gly Ile Phe Asn Lys Ala Ser Ile Gln Leu Ser Phe
                85                  90                  95
Lys Val Val Arg Leu Pro Arg Gly Pro Ser Leu Thr Phe Lys Val His
            100                 105                 110
Gln Phe Thr Leu Ala Arg Asp Val Ile Ser Leu Ser Lys Lys Gln Met
        115                 120                 125
Ile Asp Asn Asp His Phe Lys His Ala Pro Leu Val Ile Met Asn Asn
    130                 135                 140
Phe Ser Gly Asp Gly Lys His Leu Lys Leu Met Ala Thr Thr Phe Gln
145                 150                 155                 160
Asn Met Phe Pro Ser Ile Asn Leu Ala Thr Val Asn Ile Gly Thr Ile
                165                 170                 175
Arg Arg Cys Val Leu Phe Ser Tyr Asn Pro Asp Thr Lys Leu Val Glu
            180                 185                 190
Met Arg His Tyr Ser Val Gln Val Val Pro Val Gly Leu Lys Arg Ala
        195                 200                 205
Val Gln Lys Ile Val Lys Gly Thr Val Pro Asn Leu Gly Lys Cys Asn
    210                 215                 220
Glu Val Val Asp Phe Val Thr Lys Asp Gly Tyr Ala Ser Glu Ser Glu
225                 230                 235                 240
Ala Glu Asp Asp Glu Gln Ser His Val Val Leu Ala Gln Thr Leu Lys
                245                 250                 255
Ser Lys Gly Asn Leu Glu Asp Lys Lys Ser Ser Ile Lys Leu His Glu
            260                 265                 270
```

```
Ile Gly Pro Arg Leu Thr Met Gln Leu Ile Lys Ile Glu Glu Gly Leu
        275                 280                 285
Leu Thr Gly Glu Val Leu Tyr His Cys His Val Val Lys Thr Glu Asp
    290                 295                 300
Glu Lys Glu Thr Leu Arg Lys Leu Val Glu Lys Lys Arg Lys Gln Lys
305                 310                 315                 320
Glu Gln Arg Lys Lys Glu Gln Ala Glu Asn Arg Ala Phe Asn Leu Lys
                325                 330                 335
Leu Lys Lys Asp Glu Lys Trp Ala Ala Lys Arg Ala Ala Glu Gly Arg
            340                 345                 350
Thr Asp Ser Asp Pro Glu Asp Asp Ala Glu Tyr Tyr Lys Glu Glu Val
        355                 360                 365
Gly Glu Glu Pro Asp Glu Glu Leu Phe Lys Met Glu Ala Lys Ser Ser
    370                 375                 380
Arg Lys Arg Pro Ser Leu Gly Gly Gly Met Lys Tyr Lys Asn Lys Arg
385                 390                 395                 400
Ala Lys Leu Asp Thr Lys Asp Lys Asn Asp Lys Ser Glu Arg Thr Asp
                405                 410                 415
Phe Tyr Asp Arg Lys Cys Lys Phe Asp Arg Lys Asp Lys Lys Asp Lys
            420                 425                 430
Phe Asp Pro Lys Asn Gly Arg Ala Lys Phe Asp Pro Lys Asn Lys Arg
        435                 440                 445
Ala Lys Phe Asp His Pro Lys Ser Arg Lys Ser Lys
    450                 455                 460
```

<210> 18
<211> 15
<212> DNA
<213> homo sapiens

<400> 18
agggcgtcgg ggagg 15

<210> 19
<211> 358
<212> PRT
<213> mus musulus

<220>
<221> VARIANT
<222> (1)...(358)
<223> Xaa = Any Amino Acid

<400> 19

```
Phe Gly Gln Gly Gly Lys Gln Ala Ala Trp Gly Ser Pro Gly Gly Pro
 1               5                  10                  15
Asp Ile Arg Ser Ala Ile Ala Pro Gly Glu Leu Arg Asn Leu Glu Ser
            20                  25                  30
Tyr Ala Ala Gln Pro His Ser Phe Val Phe Thr Arg Gly Arg Ala Gly
        35                  40                  45
```

Arg Asn Val Arg Gln Leu Ser Leu Asp Val Arg Arg Val Met Glu Pro
50 55 60
Leu Thr Ala Thr Arg Leu Gln Val Arg Lys Lys Asn Ser Leu Lys Asp
65 70 75 80
Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His Phe Leu Ile Leu
85 90 95
Thr Lys Thr Asp Asn Ser Val Tyr Leu Lys Leu Met Arg Leu Pro Gly
100 105 110
Gly Pro Thr Leu Thr Phe Gln Ile Ser Lys Tyr Thr Leu Ile Arg Asp
115 120 125
Val Val Ser Ser Leu Arg Arg His Arg Met His Glu Gln Gln Phe Asn
130 135 140
His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro Gln Gly Met His
145 150 155 160
Ile Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn
165 170 175
Val His Thr Val Asn Leu Asn Thr Ile Lys Arg Cys Leu Leu Ile Asn
180 185 190
Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His Tyr Ser Val Lys
195 200 205
Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys Leu Leu Gln Glu
210 215 220
Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser Glu Leu Leu Ala
225 230 235 240
Thr Gly Val Gly Leu Ser Asp Ser Glu Val Glu Pro Asp Gly Glu His
245 250 255
Asn Thr Thr Glu Leu Pro Gln Ala Val Ala Gly Arg Gly Asn Met Gln
260 265 270
Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly Pro Arg Met Thr
275 280 285
Leu Gln Leu Ile Lys Ile Gln Glu Gly Val Gly Asn Gly Asn Val Leu
290 295 300
Phe His Ser Phe Val His Lys Thr Glu Glu Glu Leu Gln Ala Ile Leu
305 310 315 320
Ala Ala Lys Glu Glu Lys Leu Arg Leu Lys Ala Gln Arg Gln Asn Gln
325 330 335
Gln Ala Glu Asn Leu Gln Arg Xaa Arg Ser Cys Arg Xaa Pro Thr Arg
340 345 350
Arg Arg Ala Trp Gln Ala
355

<210> 20
<211> 137
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(137)
<223> Xaa = Any Amino Acid

<400> 20

```
Leu Gly Pro Arg Val Thr His Phe Leu Ile Leu Ser Lys Thr Glu Thr
 1               5                  10                  15
Asn Val Tyr Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr
            20                  25                  30
Phe Gly Val Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu
        35                  40                  45
Arg Arg His Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu
    50                  55                  60
Val Leu Asn Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala
65                  70                  75                  80
Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn
                85                  90                  95
Leu Asn Thr Ile Lys Arg Cys Ser Ser Xaa Asp Leu Lys Pro Gly Phe
            100                 105                 110
Pro Arg Ser Leu Asp Phe Arg Pro Ile Ile Ala Phe Lys Gly Gly Ser
        115                 120                 125
Cys Trp Ala Pro Asn Ser Gly Gly Leu
    130                 135
```

ORIGINAL U.S. SEQ LIST

Marked-up copy

SEQUENCE LISTING

<110> Welch, Peter J.
Barber, Jack R.

<120> Tumor Suppressor Molecules and Methods of Use

<130> P-IU 3446

<140> US 09/438,917
<141> 1999-11-12

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 16
<212> RNA
<213> Artificial Sequence

<220>
<223> hairpin ribozyme

<400> 1
acctccccag aaccct "u" instead of "t" 16

<210> 2
<211> 16
<212> RNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (1)...(16)
<223> n = A,T,C or G "u"

<400> 2
agggngtcgg ggaggt "u" 16

<210> 3
<211> 16
<212> RNA
<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<400> 3
agagtgtaag aaacta "u" 16

<210> 4
<211> 16
<212> RNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (1)...(16)
<223> n = A,T,C or G

<400> 4
tagtngtcta cactct 16

<210> 5
<211> 1664
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (103)...(1525)

<400> 5
gcctgatgtc gtcccacgcc gtgccggctc tcaggcgccg gaagtgagct gcgcacggcc 60
ggaagcggcg gacgcaggag gcctcgtgga ggacacagca gc atg gga cag tca 114
Met Gly Gln Ser
1

ggg agg tcc cgg cac cag aag cgc gcc ccg ccc cag gcg cag ctc cgc 162
Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln Ala Gln Leu Arg
5 10 15 20

aac ctc gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga 210
Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg
25 30 35

ggc tgc acg ggt cgc aac atc cgg cag ctc agc ctg gac gtg cgg cgg 258
Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg
40 45 50

gtc atg gag ccc gtc act gcc agc cgt ctg cag gtt cgt aag aag aac 306
Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn
55 60 65

tcg ctg aag gac tgc gtg gca gtc gct ggg ccc ctc ggg gtc aca cac 354
Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His
70 75 80

ttt ctg atc cta gca aaa caa gag acc aat gtc tac ttt aag ctg atg 402
Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr Phe Lys Leu Met
85 90 95 100

```
cgc ctc cca gga ggc ccc acc ttg acc ttc cag gtc aag aag tac tcg      450
Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser
                105                 110                 115

ctg gtg cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag      498
Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu
            120                 125                 130

cag cag ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc      546
Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro
        135                 140                 145

cat ggt atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc      594
His Gly Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe
    150                 155                 160

ccc tcc atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc      642
Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys
165                 170                 175                 180

ctc ctc atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac      690
Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His
                185                 190                 195

tat agc atc aaa gtt gtt cct gtg ggc gcg agt cgc ggg atg aag aag      738
Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys
            200                 205                 210

ctg ctc cag gag aag ttc ccc aac atg agc cgc ctg cag gac atc agc      786
Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser
        215                 220                 225

gag ctg ctg gcc acg ggc gcg ggg ctg tcg gag agc gag gca gag cct      834
Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser Glu Ala Glu Pro
    230                 235                 240

gac ggc gac cac aac atc aca gag ctg cct cag gct gtc gct ggc cgt      882
Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala Val Ala Gly Arg
245                 250                 255                 260

ggc aac atg cgg gcc cag cag agt gca gtg cgg ctc acc gag atc ggc      930
Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly
                265                 270                 275

ccg cgg atg aca ctg cag ctc atc aag gtc cag gag ggc gtc ggg gag      978
Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu Gly Val Gly Glu
            280                 285                 290

ggc aaa gtg atg ttc cac agt ttt gtg agc aag acg gag gag gag ctg     1026
Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr Glu Glu Glu Leu
        295                 300                 305

cag gcc atc ctg gaa gcc aag gag aag aag ctg cgg ctg aag gct cag     1074
```

```
Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg Leu Lys Ala Gln
    310                 315                 320

agg cag gcc cag cag gcc cag aat gtg cag cgc aag cag gag cag cgg     1122
Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys Gln Glu Gln Arg
325                 330                 335                 340

gag gcc cac aga aag aag agc ctg gag ggc atg aag aag gca cgg gtc     1170
Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys Lys Ala Arg Val
                345                 350                 355

ggg ggt agt gat gaa gag gcc tct ggg atc cct tca agg acg gcg agc     1218
Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser Arg Thr Ala Ser
            360                 365                 370

ctg gag ttg ggt gag gac gat cat gaa cag gaa gat gat gac atc gag     1266
Leu Glu Leu Gly Glu Asp Asp His Glu Gln Glu Asp Asp Asp Ile Glu
        375                 380                 385

tat ttc tgc cag gcg gtg ggc gag gcg ccc agt gag gac ctg ttc ccc     1314
Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu Asp Leu Phe Pro
    390                 395                 400

gag gcc aag cag aaa cgg ctt gcc aag tct cca ggg cgg aag cgg aag     1362
Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly Arg Lys Arg Lys
405                 410                 415                 420

cgg tgg gaa atg gat cga ggc agg ggt cgc ctt tgt gac cag aag ttt     1410
Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys Asp Gln Lys Phe
                425                 430                 435

ccc aag aca aag gac aag tcc cag gga gcc cag gcc agg cgg ggg ccc     1458
Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala Arg Arg Gly Pro
            440                 445                 450

aga ggg gct tcc cgg gat ggt ggg cga ggc cgg ggc cga ggc cgc cca     1506
Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly Arg Gly Arg Pro
        455                 460                 465

ggg aag aga gtg gcc tga g cccaagccgc accggagcag cggctggatt          1555
Gly Lys Arg Val Ala  *
    470

gaacgcccca gattggggcc cgagatgtgg ccctcggttt cctttcataa aggagttgtg   1615
tccccagccc ttccactcca gtaaagaact gaattggcaa aaaaaaaaa               1664
```

<210> 6
<211> 473
<212> PRT
<213> homo sapiens

<400> 6
Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln

```
 1               5                  10                  15
Ala Gln Leu Arg Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe
            20                  25                  30
Val Phe Thr Arg Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu
        35                  40                  45
Asp Val Arg Arg Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val
    50                  55                  60
Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu
65                  70                  75                  80
Gly Val Thr His Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr
                85                  90                  95
Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val
            100                 105                 110
Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His
        115                 120                 125
Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn
    130                 135                 140
Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala Thr Met Phe
145                 150                 155                 160
Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr
                165                 170                 175
Ile Lys Arg Cys Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu
            180                 185                 190
Asp Phe Arg His Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg
        195                 200                 205
Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu
    210                 215                 220
Gln Asp Ile Ser Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser
225                 230                 235                 240
Glu Ala Glu Pro Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala
                245                 250                 255
Val Ala Gly Arg Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu
            260                 265                 270
Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu
        275                 280                 285
Gly Val Gly Glu Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr
    290                 295                 300
Glu Glu Glu Leu Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg
305                 310                 315                 320
Leu Lys Ala Gln Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys
                325                 330                 335
Gln Glu Gln Arg Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys
            340                 345                 350
Lys Ala Arg Val Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser
        355                 360                 Asp 365
Arg Thr Ala Ser Leu Glu Leu Gly Glu Asp Asp His Glu Gln Glu Asp
    370                 375                 380
Asp Asp Ile Glu Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu
385                 390                 395                 400
Asp Leu Phe Pro Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly
                405                 410                 415
Arg Lys Arg Lys Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys
            420                 425                 430
```

Asp Gln Lys Phe Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala
435 440 445
Arg Arg Gly Pro Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly
450 455 460
Arg Gly Arg Pro Gly Lys Arg Val Ala
465 470

<210> 7
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotides

<221> misc_feature
<222> (1)...(87)
<223> n = A,T,C or G

<400> 7
cgcgtaccag gtaatatacc acggaccgaa gtccgtgtgt ttctctggtn nnnttctnnn 60
nnnnnggatc ctgtttccgc ccggttt 87

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 8
gtccgtggta tattacctgg ta 22

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 9
cgaaaccggg cggaaacagg 20

<210> 10
<211> 52
<212> RNA
<213> Artificial Sequence

<220>
<223> hairpin ribozyme

<221> misc_feature
<222> (1)...(52)
<223> n = A,T,C or G

<400> 10
nnnnnnnnag aannnnacca gagaaacaca cguuguggua uauuaccugg ua 52

<210> 11
<211> 27
<212> DNA
<213> homo sapiens

<400> 11
ccatcctaat acgactcact atagggc 27

<210> 12
<211> 43
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (1)...(42)
<223> n = A,T,C or G

<400> 12
cgatgctcct ctagactcga gggtaccacc tccccgacnc cct 43

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
ggccacgcgt cgactagtac ttttttttttt ttttttv 38

<210> 14
<211> 20
<212> DNA
<213> homo sapiens

<400> 14
cggctcaccg agatcggccc 20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 15
ggccacgcgt cgactagtac t 21

<210> 16
<211> 429
<212> PRT
<213> mus musculus

<400> 16
Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Asn Arg Ala Gln
1 5 10 15
Ala Gln Leu Arg Asn Leu Glu Ser Tyr Ala Ala Gln Pro His Ser Phe
20 25 30
Val Phe Thr Arg Gly Arg Ala Gly Arg Asn Val Arg Gln Leu Ser Leu
35 40 45
Asp Val Arg Arg Val Met Glu Pro Leu Thr Ala Thr Arg Leu Gln Val
50 55 60
Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu
65 70 75 80
Gly Val Thr His Phe Leu Ile Leu Thr Lys Thr Cys Asn Ser Val Tyr
85 90 95
Leu Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Ile
100 105 110
Ser Lys Tyr Thr Leu Ile Arg Asp Val Val Ser Ser Leu Arg Arg His
115 Phe 120 125
Arg Met His Glu Gln Gln Pro Asn His Pro Pro Leu Leu Val Leu Asn
130 135 140
Ser Phe Gly Pro Gln Ala Met His Ile Lys Leu Met Ala Thr Met Phe
145 150 155 160
Gln Asn Leu Phe Pro Ser Ile Asn Val His Thr Val Asn Leu Asn Thr
165 170 Gln 175
Ile Lys Arg Cys Leu Leu Ile Asn Tyr Asn Pro Asp Ser Cys Glu Leu
180 185 190
Asp Phe Arg His Tyr Ser Val Lys Val Val Pro Val Gly Ala Ser Arg
195 200 205
Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu
210 215 220
Gln Asp Ile Ser Glu Leu Leu Ala Thr Gln Val Gly Leu Ser Asp Ser
225 230 235 240
Glu Val Glu Pro Asp Gln Glu His Asn Ile Thr Glu Leu Pro Gln Ala
245 250 255
Val Ala Gly Arg Gly Asn Met Gln Ala Gln Gln Ser Ala Val Arg Leu
260 265 270
Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Ile Gln Glu
275 280 285
Gly Val Gly Glu Gly Asn Val Leu Phe His Ser Phe Val His Lys Thr
290 295 300
Glu Glu Glu Leu Gln Ala Ile Leu Ala Ala Lys Glu Glu Lys Leu Arg
305 310 315 320
Leu Lys Ala Gln Arg Gln Asn Gln Gln Ala Glu Asn Leu Gln Phe Ser
325 330 335

```
Arg Ser Cys Arg Gly Pro Gln Glu Glu Glu Pro Gly Arg His Lys Ala
            340                 345                 350
Ser Pro Cys Lys Gly Arg Arg Glx Gln Glx Cys Glx Gly Pro Arg Gly
        355                 360                 365
Thr Ala Arg Gly Gln Trp Gly Ala Gly Gln Pro Glu Asp Glu Glu Asp
    370                 375                 380
Asp Ala Glu Tyr Phe Arg Gln Ala Val Gly Glu Glu Pro Asp Glu Asp
385                 390                 395                 400
Leu Phe Pro Thr Ala Ala Lys Arg Arg Arg Gln Gly Gly Leu Leu Ala
                405                 410                 415
Lys Lys Gln Arg Gly Phe Glu Gln Arg Pro Gly Asn Lys
            420                 425
```

<210> 17
<211> 460
<212> PRT
<213> Drosophila

<400> 17

```
Met Gly Gly Lys Lys Lys Val His Pro Lys Thr Arg Thr Ala Ala Phe
 1               5                  10                  15
Lys Ala Ser Glu Pro Ser Glu Ile Val Glu Ala Pro His Ser Phe Val
            20                  25                  30
Ile His Arg Gly Leu Ala Cys Pro Tyr Ile Thr Asp Leu Thr Leu Asp
        35                  40                  45
Phe Arg Arg Ile Met Glu Pro Phe Thr Ala Ser Asn Leu Arg Glu Lys
    50                  55                  60
Arg Met Asn Arg Ile Gln Asp Phe Val Cys Leu Ser Ser Phe Phe His
65                  70                  75  Ile             80
Val Ser His Met Gly Ile Phe Asn Lys Ala Ser Thr Gln Leu Ser Phe
                85                  90                  95
Lys Val Val Arg Leu Pro Arg Gly Pro Ser Leu Thr Phe Lys Val His
            100                 105                 110
Gln Phe Thr Leu Ala Arg Asp Val Ile Ser Leu Ser Lys Lys Gln Met
        115                 120                 125
Ile Asp Asn Asp His Phe Lys His Ala Pro Leu Val Ile Met Asn Asn
    130                 135                 140
Phe Ser Gly Asp Gly Lys His Leu Lys Leu Met Ala Thr Thr Phe Gln
145                 150                 155                 160
Asn Met Phe Pro Ser Ile Asn Leu Ala Thr Val Asn Ile Gly Thr Ile
                165                 170                 175
Arg Arg Cys Val Leu Phe Ser Tyr Asn Pro Asp Thr Lys Leu Val Glu
Arg         180                 185                 190
Met Pro His Tyr Ser Val Gln Val Val Pro Val Gly Leu Lys Arg Ala
        195                 200                 205
Val Gln Lys Ile Val Lys Gly Thr Val Pro Asn Leu Gly Lys Cys Asn
    210                 215                 220
Glu Val Val Asp Phe Val Thr Lys Asp Gly Tyr Ala Ser Glu Ser Glu
225                 230                 235                 240
Ala Glu Asp Asp Glu Gln Ser His Val Val Leu Ala Gln Thr Leu Lys
                245                 250                 255
Ser Lys Gly Asn Leu Glu Asp Lys Lys Ser Ser Ile Lys Leu His Glu
            260                 265                 270
```

Ile Gly Pro Arg Leu Thr Met Gln Leu Ile Lys Ile Glu Glu Gly Leu
275 Leu 280 Cys 285
Leu Thr Gly Glu Val Ile Tyr His Asp His Val Val Lys Thr Glu Asp
290 295 300
Glu Lys Glu Thr Leu Arg Lys Leu Val Glu Lys Lys Arg Lys Gln Lys
305 310 315 Phe 320
Glu Gln Arg Lys Lys Glu Gln Ala Glu Asn Arg Ala Arg Asn Leu Lys
325 330 335
Leu Lys Lys Asp Glu Lys Trp Ala Ala Lys Arg Ala Ala Glu Gly Arg
340 345 350
Thr Asp Ser Asp Pro Glu Asp Asp Ala Glu Tyr Tyr Lys Glu Glu Val
355 360 365
Gly Glu Glu Pro Asp Glu Glu Leu Phe Lys Met Glu Ala Lys Ser Ser
370 375 380
Arg Lys Arg Pro Ser Leu Gly Gly Gly Met Lys Tyr Lys Asn Lys Arg
385 390 395 400
Ala Lys Leu Asp Thr Lys Asp Lys Asn Asp Lys Ser Glu Arg Thr Asp
Phe 405 Cys 410 415
Lys Tyr Asp Arg Lys Asp Lys Phe Asp Arg Lys Asp Lys Lys Asp Lys
420 425 430
Phe Asp Pro Lys Asn Gly Arg Ala Lys Phe Asp Pro Lys Asn Lys Arg
435 Pro 440 445
Ala Lys Phe Asp His Arg Lys Ser Arg Lys Ser Lys
450 455 460

<210> 18
<211> 15
<212> DNA
<213> homo sapien

<400> 18
agggcgtcgg ggagg 15

<210> 19
<211> 358
<212> PRT
<213> mus musulus

<220>
<221> VARIANT
<222> (1)...(358)
<223> Xaa = Any Amino Acid

<400> 19
Phe Gly Gln Gly Gly Lys Gln Ala Ala Trp Gly Ser Pro Gly Gly Pro
1 5 10 15
Asp Ile Arg Ser Ala Ile Ala Pro Gly Glu Leu Arg Asn Leu Glu Ser
20 25 30
Tyr Ala Ala Gln Pro His Ser Phe Val Phe Thr Arg Gly Arg Ala Gly
35 40 45
Arg Asn Val Arg Gln Leu Ser Leu Asp Val Arg Arg Val Met Glu Pro
50 55 60
Leu Thr Ala Thr Arg Leu Gln Val Arg Lys Lys Asn Ser Leu Lys Asp

```
65                  70                  75                  80
Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His Phe Leu Ile Leu
                85                  90                  95
Thr Lys Thr Asp Asn Ser Val Tyr Leu Lys Leu Met Arg Leu Pro Gly
            100                 105                 110
Gly Pro Thr Leu Thr Phe Gln Ile Ser Lys Tyr Thr Leu Ile Arg Asp
        115                 120                 125
Val Val Ser Ser Leu Arg Arg His Arg Met His Glu Gln Gln Phe Asn
    130                 135                 140                 His
His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro Gln Gly Met Lys
145                 150                 155                 160
Ile Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn
                165                 170                 175
Val His Thr Val Asn Leu Asn Thr Ile Lys Arg Cys Leu Leu Ile Asn
            180                 185                 190
Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His Tyr Ser Val Lys
        195                 200                 205
Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys Leu Leu Gln Glu
    210                 215                 220
Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser Glu Leu Leu Ala
225                 230                 235                 240
Thr Gly Val Gly Leu Ser Asp Ser Glu Val Glu Pro Asp Gly Glu His
                245                 250                 255
Asn Thr Thr Glu Leu Pro Gln Ala Val Ala Gly Arg Gly Asn Met Gln
            260                 265                 270
Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly Pro Arg Met Thr
        275                 280                 285
Leu Gln Leu Ile Lys Ile Gln Glu Gly Val Gly Asn Gly Asn Val Leu
    290                 295                 300
Phe His Ser Phe Val His Lys Thr Glu Glu Glu Leu Gln Ala Ile Leu
305                 310                 315                 320
Ala Ala Lys Glu Glu Lys Leu Arg Leu Lys Ala Gln Arg Gln Asn Gln
                325                 330                 335
Gln Ala Glu Asn Leu Gln Arg Xaa Arg Ser Cys Arg Xaa Pro Thr Arg
            340                 345                 350
Arg Arg Ala Trp Gln Ala
        355

<210> 20
<211> 137
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(137)
<223> Xaa = Any Amino Acid

<400> 20
Leu Gly Pro Arg Val Thr His Phe Leu Ile Leu Ser Lys Thr Glu Thr
1               5                   10                  15
Asn Val Tyr Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr
            20                  25                  30
```

```
Phe Gln Val Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu
    35                  40                  45
Arg Arg His Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu
50                  55                  60
Val Leu Asn Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala
65                  70                  75                  80
Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn
                85                  90                  95
Leu Asn Thr Ile Lys Arg Cys Ser Ser Xaa Asp Leu Lys Pro Gly Phe
            100                 105                 110
Pro Arg Ser Leu Asp Phe Arg Pro Ile Ile Ala Phe Lys Gly Gly Ser
        115                 120                 125
Cys Trp Ala Pro Asn Ser Gly Gly Leu
    130                 135
```